

OM nucleic - nucleic search, using sw model

Run on: June 16, 2010, 20:11:08 ; Search time 1293 Seconds
(without alignments)
93164.247 Million cell updates/sec

Title: US-10-593-202-1_COPY_54755_55810
Perfect score: 1056
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21196085 seqs, 57036634027 residues

Total number of hits satisfying chosen parameters: 42392170

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 17: gb_tsa:*
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 20: gb_vrt:*

SUMMARIES

Result No.	Query			DB	ID	Description
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1	1056	100.0	11928	9	CS175724	CS175724 Sequence
2	1056	100.0	11928	9	CS433133	CS433133 Sequence
3	1056	100.0	100140	9	CS175723	CS175723 Sequence
4	1056	100.0	100140	9	CS433132	CS433132 Sequence
C	1056	100.0	185146	14	AC159967	AC159967 Mus muscu
C	1056	100.0	230474	14	AC102564	AC102564 Mus muscu
7	1042.4	98.7	11539	9	CS175727	CS175727 Sequence
8	1042.4	98.7	11539	9	CS433136	CS433136 Sequence
9	1042.4	98.7	15913	14	AF235496S4	AF235499 Mus muscu
10	896.2	84.9	938	14	AF189741	AF189741 Mus muscu
11	547.4	51.8	560	9	CS175725	CS175725 Sequence
12	547.4	51.8	560	9	CS433134	CS433134 Sequence

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ALIGNMENTS

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LOCUS CS175724 11928 bp DNA linear PAT 12-OCT-2005
DEFINITION Sequence 2 from Patent WO2005090559.
ACCESSION CS175724
VERSION CS175724.1 GI:77627140
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Rohrschneider, L.R.
TITLE Methods and compositions involving s-ship promoter regions
JOURNAL Patent: WO 2005090559-A 2 29-SEP-2005;
Fred Hutchinson Cancer Research Center (US)
FEATURES
source Location/Qualifiers
1. .11928
/organism="Mus musculus"
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/db_xref="taxon:10090"

ORIGIN

Query Match 100.0%; Score 1056; DB 9; Length 11928;
Best Local Similarity 100.0%;
Matches 1056; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	481	CTCCATAACATAAAAGTGTGATGGAGAAAAGGCACCTAAATGTCAACCTCAAAACCCCTACCTG	540
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QY	601	CACACACACACACAAAATAAAATAAGTAAATAAAATAATTTAGCTCTCCAGACCAAATC	660
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Db	6286	TTGGTGA AAACCCATGCA TTTTGCA TTTGTGTGTCTCTACAAACACTGAAAGGTTAAGAAGC	6345
QY	721	ATGCTCCTTAGTAAATTTTATAGCAGTTTTCGTTTCCAGATTGAAAACAGATTCTATAGGC	780
Db	6346	ATGCTCCTTAGTAAATTTTATAGCAGTTTTCGTTTCCAGATTGAAAACAGATTCTATAGGC	6405
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QY	841	GTCGGGGTCTGGGCCAGGATGACGGGGCCAACTGATCTTTGCCGGGGCTTGTCCTTCAGGG	900
Db	6466	GTCGGGGTCTGGGCCAGGATGACGGGGCCAACTGATCTTTGCCGGGGCTTGTCCTTCAGGG	6525
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Db 6646 GTCATCAGGACTCTGCCATCCCTGGAGTCTCTGCAG 6681

RESULT 2

CS433133

LOCUS CS433133 11928 bp DNA linear PAT 19-OCT-2006

DEFINITION Sequence 2 from Patent WO2006102188.

ACCESSION CS433133

VERSION CS433133.1 GI:116286367

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Rohrschneider, L.R.

TITLE Methods and compositions involving the s-ship promoter

JOURNAL Patent: WO 2006102188-A 2 28-SEP-2006;

Fred Hutchinson Cancer Research Center (US)

FEATURES

source

1. .11928

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

ORIGIN

Query Match 100.0%; Score 1056; DB 9; Length 11928;

100.00

Best Local Similarity 100.0%;

Matches 1056; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	5626	CAC	TTC	CAG	CTT	CCT	T	T	A	T	C	A	T	T	T	A	A	A	A	A	A	T	T	C	C	T	A	T	G	T	G	A	C	T	A	C	T	G	T	A	T	T	A	A	A	T	5685																	
Qy	61	CAC	CAC	ACG	GC	CA	A	T	A	C	T	C	C	C	C	C	C	C	C	C	C	A	A	C	T	C	C	C	T	C	T	A	C	C	C	A	A	T	T	C	C	C	A	A	T	T	C	120																
Db	5686	CAC	CAC	ACG	GC	CA	A	T	A	C	T	C	C	C	C	C	C	C	C	C	C	A	A	C	T	C	C	C	T	C	T	A	C	C	C	A	A	T	T	C	C	C	A	A	T	T	C	5745																
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Qy	541	CATGTGCACACACATACATCCAC	600
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Qy	601	CACACACACACACAAATAAAATAAGTAAATAAAATAAAATAATTTAGCTCTCCAGACCCAAATC	660
Db	6226	CACACACACACACAAATAAAATAAGTAAATAAAATAATTTAGCTCTCCAGACCCAAATC	6285
Qy	661	TTGGTGAAACCCCATGCAATTTGCATTTGTGTGTCTCTACAAACACTGAAGGTTAAGAAGC	720
Db	6286	TTGGTGAAACCCCATGCAATTTGCATTTGTGTGTCTCTACAAACACTGAAGGTTAAGAAGC	6345
Qy	721	ATGCTCCTTAGTAATTTTATAGCAGTTTGCGTTTCCAGATTGAAAAACAGATTCTATAGGC	780
Db	6346	ATGCTCCTTAGTAATTTTATAGCAGTTTGCGTTTCCAGATTGAAAAACAGATTCTATAGGC	6405
Qy	781	TACACAGTGCTAAATGGATTATGCTCAGATACAGATTGAAAAAGGATACAGATTGAAAAGG	840
Db	6406	TACACAGTGCTAAATGGATTATGCTCAGATACAGATTGAAAAAGGATACAGATTGAAAAGG	6465
Qy	841	GTCGGGGTCTGGGCCAGGATGACGGGCCCAACTGATCTTTGCCGGGGCTTGTCCTTCAGGG	900
Db	6466	GTCGGGGTCTGGGCCAGGATGACGGGCCCAACTGATCTTTGCCGGGGCTTGTCCTTCAGGG	6525
Qy	901	AAGGGTTACAGGATTACCCACTGGGGTGTGGCCTATCTGTGTTAGGACCTGAATTGCCT	960
Db	6526	AAGGGTTACAGGATTACCCACTGGGGTGTGGCCTATCTGTGTTAGGACCTGAATTGCCT	6585

Qy	961	GGAGTGTTTCTAGTTCCCACTAGTTGTTGAACTTTACCTTGAACCTCTGCTCCCAGGGAA	1020
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DEFINITION	Sequence 1 from Patent WO2005090559.			PAT 12-OCT-2005

CS175723
 CS175723.1 GI:77627139
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 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Rohrschneider, L.R.
TITLE Methods and compositions involving s-ship promoter regions
JOURNAL Patent: WO 2005090559-A 1 29-SEP-2005;
Fred Hutchinson Cancer Research Center (US)

FEATURES

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QY	661	TTGGTGAAACCCATGCATTTGCATTTGTGTGTCTCTACAAACACTGAAGGTTAAGAAAGC	720
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Db	55475	ATGCTCCTTAGTAATTTTATAGCAGTTTGCGTTTCCAGATTGAAAAACAGATTCTATAGGC	55534
QY	781	TACACAGTGCTAAATGGATTATGCTCAGATACAGATTGAAAAAGGATACAGATTGAAAAGG	840
Db	55535	TACACAGTGCTAAATGGATTATGCTCAGATACAGATTGAAAAAGGATACAGATTGAAAAGG	55594
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DEFINITION      Sequence 1 from Patent WO2006102188.
ACCESSION      CS433132
VERSION        CS433132.1   GI:116286366
KEYWORDS       .
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
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               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1
AUTHORS        Rohrschneider,L.R.
TITLE          Methods and compositions involving the s-ship promoter
JOURNAL        Patent: WO 2006102188-A 1 28-SEP-2006;
               Fred Hutchinson Cancer Research Center (US)
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misc_feature

27350. .78168

/note="N = A, C, G OR T/U"

ORIGIN

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Best Local Similarity 100.0%;
Matches 1056; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CACTTCCAGCTTCCTTTATCATTTTAAAAAGAAATTTCCTATGTGACTACTGTATTAAAT 60
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Qy 61 CACCACACGGCCAAATACTCCCCCCTCCCTCCCAAAATCCCTCTACCCACTCAAATTC 120
Db 54815 CACCACACGGCCAAATACTCCCCCCTCCCTCCCAAAATCCCTCTACCCACTCAAATTC 54874
Qy 121 TTATCTTGATTCTTTATCATTTATATACATATGTGTATATATATGTGTGTATATATA 180
Db 54875 TTATCTTGATTCTTTATCATTTATATACATATGTGTATATATGTGTGTGTATATATA 54934
Qy 181 TATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTGTTGCATGTTTCAA 240
Db 54935 TATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTGTTGCATGTTTCAA 54994
Qy 241 TGTGCTTTCACGAGGCTGGGGGATGGCTCAGTGGGCAAAATTCAGCTGCACAAGCCT 300
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Qy	361	TACTAGCATGCTTGCTGGAAAGCAAAAGACAGGGAATCCCCTGGAGACTTAGAATCTCAGAAG	420
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Qy	421	TGATCTGGGCTGGACAGACTAGCTGAACCTGGCCAGCTCTGGGTTTCATCAAGAAAACCCCTAC	480
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Qy	541	CATGTGCACACACATACATCCAC	600
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Qy	601	CACACACACACACAAATAAAATAAGTAAATAAAATAAAATAATTTAGCTCTCCAGACCAAATC	660
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Qy	661	TTGGTGAAACCCCATGCAATTTGCATTTGTGTGTGTCTTACAAAACACTGAAAGGTTAAGAAGC	720
Db	55415	TTGGTGAAACCCCATGCAATTTGCATTTGTGTGTGTCTTACAAAACACTGAAAGGTTAAGAAGC	55474
Qy	721	ATGCTCCTTAGTAATTTTATAGCAGTTTGGCGTTTCCAGATTGAAAACAGATTCTATAGGC	780
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Qy	781	TACACAGTGCTAAATGGATTATGCTCAGATACAGATTGAAAAGGATACAGATTGAAAAGG	840
Db	55535	TACACAGTGCTAAATGGATTATGCTCAGATACAGATTGAAAAGGATACAGATTGAAAAGG	55594
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Db	55595	GTGGGGTCTGGGCCAGGATGACGGGCCAACTGATCTTTGCCGGGCTTGTCCTTCAGGG	55654
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RESULT 5				
AC159967/c				
LOCUS	AC159967	185146 bp	DNA	linear ROD 10-AUG-2005
DEFINITION	Mus musculus chromosome 1, clone RP23-302P9, complete sequence.			
ACCESSION	AC159967			
VERSION	AC159967.2	GI:72096116		
KEYWORDS	HTG.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
	Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 185146)			
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.			
TITLE	Mus musculus chromosome 1, clone RP23-302P9			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 185146)			

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
 Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
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 Zimmer,A. and Zody,M.

TITLE

Direct Submission

JOURNAL

Submitted (14-APR-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 185146)

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
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Zimmer,A. and Zody,M.

TITLE

JOURNAL

Direct Submission

Submitted (10-AUG-2005) Broad Institute of MIT and Harvard, 320

Charles Street, Cambridge, MA 02141, USA

On Aug 10, 2005 this sequence version replaced gi:62543423.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Broad Institute of MIT and Harvard

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@broad.mit.edu

----- Project Information

Center project name: J5628

Center clone name: 302_P_9

Some of the sequence contained within base pairs 1 - 61047 was
stolen from accession AC102630

Some of the sequence contained within base pairs 75127 to the end

of the clone was stolen from accession AC102564.

FEATURES

source

Location/Qualifiers

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/chromosome="1"

/map="1"

/clone="RP23-302P9"

/clone_lib="RPCI-23 Female Mouse BAC"

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Qy	361	TACTAGCATGCTTGCTGGAAGCAAAACAGAGGGAATCCCTGGAGACTTAGAATCTCAGAAG	420
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Qy	661	TTGGTGAAACCCATGCAATTTGCAATTTGTGTGTCTTACAAACACTGAAAGGTTAAGAAGC	720
Db	87521	 TTGGTGAAACCCATGCAATTTGCAATTTGTGTGTCTTACAAACACTGAAAGGTTAAGAAGC	87462
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Qy	1021	GTCATCAGGACTCTGCCATCCCTGGAGTCTCTGCAG	1056
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AC102564/c

AC102564 230474 bp DNA linear ROD 21-JAN-2005

LOCUS Mus musculus chromosome 1, clone RP23-210C12, complete sequence.

DEFINITION

AC102564

AC102564.7 GI:58000610

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 230474)

Birren,B., Nusbaum,C. and Lander,E.

Mus musculus chromosome 1, clone RP23-210C12

Unpublished

2 (bases 1 to 230474)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
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Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

TITLE
 JOURNAL

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 230474)

REFERENCE

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,
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 Zimmer, A. and Zody, M.

Direct Submission

TITLE
 JOURNAL

Submitted (10-DEC-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 230474)

REFERENCE

REFERENCE	4 (bases 1 to 230474)
AUTHORS	Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE	Direct Submission
JOURNAL	Submitted (21-JAN-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Jan 21, 2005 this sequence version replaced gi:55831552. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html ----- Genome Center Center: Broad Institute of MIT and Harvard Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: genome@genome.washington.edu

Contact: sequence_submissions@broad.mit.edu

----- Project Information

Center project name: L19015

Center clone name: 210_C_12

FEATURES

Location/Qualifiers

source

1. .230474

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="1"

/map="1"

/clone="RP23-210C12"

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Qy	61	CACCACACGGCCAAATACTCCCCCCTCCCTCCCAAAATCCCTCTACCCACTCAAATTC	120		
Db	12995	CACCACACGGCCAAATACTCCCCCCTCCCTCCCAAAATCCCTCTACCCACTCAAATTC	12936		
Qy	121	TTATCTTGTATTCTTTATCATTTATTACATAATGTGTATATATATGTGTGTGTATATATA	180		
Db	12935	TTATCTTGTATTCTTTATCATTTATTACATAATGTGTATATATGTGTGTGTATATATA	12876		
Qy	181	TATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTTGTTGCATGTTTCAA	240		
Db	12875	TATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTTGTTGCATGTTTCAA	12816		
Qy	241	TGTGCTTTCACGAGGCTGGGGGGATGGCTCAGTGGGCAAAATTCAGCTGCACAAGCCT	300		
Db	12815	TGTGCTTTCACGAGGCTGGGGGGATGGCTCAGTGGGCAAAATTCAGCTGCACAAGCCT	12756		
Qy	301	AAGGACCAGGTTTCAGATCCCCCAATATAAAAGCTGGCTGGACATGGTGGCTTGCCCTATGA	360		
Db	12755	AAGGACCAGGTTTCAGATCCCCCAATATAAAAGCTGGCTGGACATGGTGGCTTGCCCTATGA	12696		
Qy	361	TACTAGCATGCTTGCTGGAAGCAAAAGACAGGGAATCCCTGGAGACTTAGAATCTCAGAAG	420		
				

		12695	TACTAGCATGCTTGCTGGAAAGCAAAAGACAGGGAATCCCTGGAGACTTAGAATCTCAGAAG	12636
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		421	TGATCTGGGCTGGACAGACTAGCTGAACCTGGCCAGCTCTGGGTTTCATCAAGAAACCCCTAC	480
Qy				
		12635	TGATCTGGGCTGGACAGACTAGCTGAACCTGGCCAGCTCTGGGTTTCATCAAGAAACCCCTAC	12576
Db				
		481	CTCCATAACATAAAAGTGTGATGGAGAAAGGCACCTAAATGTCAACCTCAAAACCCCTACCTG	540
Qy				
		12575	CTCCATAACATAAAAGTGTGATGGAGAAAGGCACCTAAATGTCAACCTCAAAACCCCTACCTG	12516
Db				
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Qy				
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		12455	CACACACACACACAAAATAAATAAGTAAATAAATAAATTTAGCTCTCCAGACCAAATC	12396
Db				
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Qy				
		12395	TGGTGAAACCCATGCATTTGTCATTTGTGTGTCTCTACAAACACTGAAAGGTTAAGAAGC	12336
Db				
		721	ATGCTCCTTAGTAATTTTATAGCAGTTTTCGTTTCCAGATTGAAAACAGATTCTATAGGC	780
Qy				
		12335	ATGCTCCTTAGTAATTTTATAGCAGTTTTCGTTTCCAGATTGAAAACAGATTCTATAGGC	12276
Db				
		781	TACACAGTGTAAATGGATTATGCTCAGATACAGATTGAAAAGGATACAGATTGAAAAGG	840
Qy				
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Db				
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Qy				
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Db      12215  GTCGGGGTCTGGGCCAGGATGACGGGGCCAACTGATCTTTGCCGGGGCTTGTCTTCAGGG 12156

QY      901   AAGGGTTACAGGATTCAACCACTGGGGTGTGGCCTATCTGCTGTTAGGACCTGAATTGCCT 960
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Db      12155  AAGGGTTACAGGATTCAACCACTGGGGTGTGGCCTATCTGCTGTTAGGACCTGAATTGCCT 12096

QY      961   GGAGTGTTTCTAGTTCCTCCACTAGTTGTTGAACTTTACCTTGAACTCTGCTCCCAGGGAA 1020
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Db      12095  GGAGTGTTTCTAGTTCCTCCACTAGTTGTTGAACTTTACCTTGAACTCTGCTCCCAGGGAA 12036

QY      1021  GTCATCAGGACTCTGCCATCCCTGGAGTCTCTGCAG 1056
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Db      12035  GTCATCAGGACTCTGCCATCCCTGGAGTCTCTGCAG 12000

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RESULT 7
CS175727
LOCUS      CS175727          11539 bp      DNA          linear      PAT 12-OCT-2005
DEFINITION Sequence 5 from Patent WO2005090559.
ACCESSION  CS175727
VERSION    CS175727.1  GI:77627143
KEYWORDS   .
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Rohrschneider, L.R.
TITLE      Methods and compositions involving s-ship promoter regions
JOURNAL    Patent: WO 2005090559-A 5 29-SEP-2005;
            Fred Hutchinson Cancer Research Center (US)
FEATURES   Location/Qualifiers
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/organism="Mus musculus"
/mol_type="unassigned DNA"
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ORIGIN

Query Match	98.7%;	Score 1042.4;	DB 9;	Length 11539;
Best Local Similarity	99.8%;			
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Qy	1	CACTTCCAGCTTCCTTTATCATTTTAAAAAGAAATTCCTATGTGACTACTGTATTTAAAT	60
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Qy	61	CACCACACGGCCAAATACTCCCCCCTCCCTCCCAAATCCCTCTACCCACTCAAATTC	120
Db	5331	CACCACACGGCCAAATACTCCCCCCTCCCTCCCAAATCCCTCTACCCACTCAAATTC	5390

Qy	121	TTATCTTGTAATCTTTATCATTTATATACATATGTGTATATATGTGTGTGTATATATA	180
Db	5391	TTATCTTGTAATCTTTATCATTTATATACATATGTGTATATATGTGTGTGTATATATA	5450

Qy	181	TATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTGTTGCATGTTTCAA	240
Db	5451	TATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTGTTGCATGTTTCAA	5510

Qy	241	TGTGCTTTCACGAGGCTGGGGGATGGCTCAGTGGCAAAATTCAGCTGCACAAAGCCT	300
Db	5511	TGTGCTTTCACGAGGCTGGGGGATGGCTCAGTGGCAAAATTCAGCTGCACAAAGCCT	5570

Qy	301	AAGGACCAGGGTTCAGATCCCCCAATATAAAGGCTGGCTGGACATGGTGGCTTGCCCTATGA	360
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Qy	841	GTCGGGGTCTGGGCCAGGATACGGGGCCAACTGATCTTTGCCGGGGCTTGTCCTTCAGGG	900
Db	6111	GTCGGGGTCTGGGCCAGGATACGGGGCCAACT-ATCTTTGCCCGGGCTTGTCCTTCAGGG	6169
Qy	901	AAGGGTTACAGGATTACCACTGGGGTGTGGCCTATCTGCTGTTAGGACCTGAATTGCCT	960
Db	6170	AAGGGTTACAGGATTACCACTGGGGTGTGGCCTATCTGCTGTTAGGACCTGAATTGCCT	6229
Qy	961	GGAGTGTCTTAGTTCCCACTAGTTGTTGAACTTTACCTTGAACCTCTGCTCCAGGGAA	1020
Db	6230	GGAGTGTCTTAGTTCCCACTAGTTGTTGAACTTTACCTTGAACCTCTGCTCCAGGGAA	6289
Qy	1021	GTCATCAGGACTCTGCCATCCCTGGAGTCTCTGCAG	1056
Db	6290	GTCATCAGGACTCTGCCATCCCTGGAGTCTCTGCAG	6325

RESULT 8

CS433136

LOCUS	CS433136	11539 bp	DNA	linear	PAT 19-OCT-2006
DEFINITION	Sequence 5 from Patent WO2006102188.				

ACCESSION CS433136

VERSION CS433136.1 GI:116286370

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Rohrschneider, L.R.

TITLE Methods and compositions involving the s-ship promoter

JOURNAL Patent: WO 2006102188-A 5 28-SEP-2006;

Patent: WO 2006102188-A 5 28-SEP-2006;

Fred Hutchinson Cancer Research Center (US)

FEATURES

Location/Qualifiers

source

1. .11539

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/db_xref="taxon:10090"

misc_feature

1847

/note="N = A, C, G OR T/U"

ORIGIN

Query Match 98.7%; Score 1042.4; DB 9; Length 11539;

Best Local Similarity 99.8%;

Matches 1054; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY      121 TTATCTTGTATTCTTTATCATTTATACATAATGTGTATATATGTGTGTGTATATATA 180
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Db	6170	AAGGGTTA	CAGGATTCACCACTGGGGTGTGGCCTATCTGCTGTAGGACCTGAATTGCCT	6229
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Db	6230	GGAGTGTT	TCTAGTTCCTCCACTAGTTGTTGAACTTTACCTTGAACTCTGCTCCCAGGGAA	6289
Qy	1021	GTCATCAG	GAAGTCTGCCATCCCTGGAGTCTCTGCAG	1056
Db	6290	GTCATCAG	GAAGTCTGCCATCCCTGGAGTCTCTGCAG	6325

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DEFINITION	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 3 through 6.			
ACCESSION	AF235499			
VERSION	AF235499.1 GI:10863172			
KEYWORDS	.			
SEGMENT	4 of 7			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 15913)
WOLF, I., Lucas, D.M., Algate, P.A. and Rohrschneider, L.R.
Cloning of the genomic locus of mouse SH2 containing inositol
5-phosphatase (SHIP) and a novel 110-kDa splice isoform, SHIPdelta
Genomics 69 (1), 104-112 (2000)
11013080
2 (bases 1 to 15913)
WOLF, I.B., Lucas, D.M., Algate, P.A. and Rohrschneider, L.R.
Direct Submission
Submitted (17-FEB-2000) Division of Basic Sciences, Fred Hutchinson
Cancer Research Center, 1100 Fairview Ave N, Seattle, WA
98109-1024, USA

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exon

exon

exon

exon

ORIGIN

Matches 1054; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy	421	TGATCTGGCTGGACAGACTAGCTGAACCTGGCCAGCTCTGGGTTTCATCAAGAAACCCCTAC	480
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Qy	481	CTCCATAACATAAAAGTGTGATGGAGAAAAGGCACCTAATGTCAACCTCAAAACCCCTACCTG	540
Db	14020	CTCCATAACATAAAAGTGTGATGGAGAAAAGGCACCTAATGTCAACCTCAAAACCCCTACCTG	14079
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Db	14080	CATGTGCACACACATACATCCAC	14139
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Qy	661	TTGGTGAAACCCCATGTCATTTGTCATTTGTGTGTGTCCTACAAAACACTGAAAGGTTAAGAAGC	720
Db	14200	TTGGTGAAACCCCATGTCATTTGTCATTTGTGTGTGTCCTACAAAACACTGAAAGGTTAAGAAGC	14259
Qy	721	ATGCTCCTTAGTAATTTTATAGCAGTTTGCGTTTCCAGATTGAAAAACAGATTCTATAGGC	780
Db	14260	ATGCTCCTTAGTAATTTTATAGCAGTTTGCGTTTCCAGATTGAAAAACAGATTCTATAGGC	14319
Qy	781	TACACAGTGTCTAAATGGATTATGCTCAGATACAGATTGAAAAAGGATACAGATTGAAAAAGG	840
Db	14320	TACACAGTGTCTAAATGGATTATGCTCAGATACAGATTGAAAAAGGATACAGATTGAAAAAGG	14379
Qy	841	GTCGGGGTCTGGGCCAGGATGACGGGGCCAACTGATCTTTGCCGGGGGCTTGTCCTTCAGGG	900
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Qy	901	AAGGGTTACAGGATTACCACTGGGGTGTGGCCTATCTGCTGTTAGGACCTGAATTGCCT	960
Db	14439	AAGGGTTACAGGATTACCACTGGGGTGTGGCCTATCTGCTTAGGACCTGAATTGCCT	14498
Qy	961	GGAGTGTTTCTAGTTCCCACTAGTTGTTGAACTTTACCTTGAACTCTGCTCCCAGGAA	1020
Db	14499	GGAGTGTTTCTAGTTCCCACTAGTTGTTGAACTTTACCTTGAACTCTGCTCCCAGGAA	14558
Qy	1021	GTCATCAGGACTCTGCCATCCCCTGGAGTCTCTGCAG	1056
Db	14559	GTCATCAGGACTCTGCCATCCCCTGGAGTCTCTGCAG	14594

[illegible]

REFERENCE 2 (bases 1 to 938)
AUTHORS Tu,Z. and Kerr,W.G.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1999) Cell and Molecular Biology, University of Pennsylvania, 1318 Blockley Hall, 418 Guardian Drive, Philadelphia, PA 19104, USA

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source Location/Qualifiers
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Query Match 84.9%; Score 896.2; DB 14; Length 938;
Best Local Similarity 97.9%;
Matches 921; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

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Db	61	ATTCTTATCTTGTATTCTTTATCATTTATATACATATGTGTATATGTGTGTGTATA	120
Qy	177	TATATATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCATTGTCATGTTT	236
		

Db	121	TATATATACTATACTACTGCTAATGAGTAACATTTAGTGTATTATTCATTGNTGCTTT	180
QY	237	TCAATGTGCTTTCAGGAGGCTGGGGGGATGGCTCAGTGGGCAAAATTTAGTGCACAA	296
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QY	297	GCCTAAGGACCAGGTTTCAGATCCCCAATATAAAGCTGGCTGGACATGGTGGCTTGCCT	356
Db	241	GCCTAAGGACCAGGTTTCAGATCCCCAATATAAAGCTGGCTGGACATGGGGGCTTGCCT	300
QY	357	ATGATACTAGCATGCTTGCTGGAAGCAAAAGACAGGGAATCCCTGGAGACTTAGAATCTCA	416
Db	301	ATGATACTAGCATGCTTGCTGGAAGCAAAAGACAGGGAATCCCTGGAGACTTANAATCTCA	360
QY	417	GAAGTGATCTGGGCTGGACAGACTAGCTGAACTGGCCAGCTCTGGGTTTCATCAAGAAACC	476
Db	361	NAAGTGATCTGGGCTGGACAGACTAGCTGAACTGGCCAGCTCTGGGTTTCATNAANAACC	420
QY	477	CTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCTAATGTCAACCTCAAAACCCCTA	536
Db	421	CTNCCTCCATAACATAAAGTGTGANGGANAAGGCACCTAATGTCAACCTCAAAACCCCTA	480
QY	537	CCTGCATGTGCACACACATACATCCACACCACACACACACACACACACACACACAC	596
Db	481	CCTGCATGTGCACACACATACATCCACAC--CACACACACACGCACACACACACACAC	538
QY	597	CACACACACACACACAAATAAAATAAGTAAATAAAATAATTTAGCTCTCCAGACCA	656
Db	539	CACACACACACACACAAATAAAATAAGTAAATAAAATAATTTAGCTCTCCAGACCA	598
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Db	599	AATCTTGGTGAACCCCATGCATT	TGCA	TTTG	TGTG	TCTC	TACAA	CAC	TGAAG	TTAAG	658
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Qy	777	AGGCTACACAGTGCTAAAT	GGATTAT	GTCT	CAGAT	ACAG	ATTG	AAA	AGG	ATACAGATTGAA	836
Db	719	AGGCTACACAGTGCTAAAT	GGATTAT	GTCT	CAGAT	ACAG	ATTG	AAA	AGG	ATACAGATTGAA	778
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Qy	897	AGGGAAGGGTTACAGGAT	TCAC	CACT	GGGG	TGTG	GCCT	ATCT	GTGT	TAGGACCTGAATT	956
Db	838	AGGGAAGGGTTACAGGAT	TCAC	CACT	GGGG	TGTG	GCCT	ATCT	GTGT	TAGGACCTGAATT	897
Qy	957	GCCTGGAGTGT	TTCTAG	TCCC	ACTAG	TTGTT	GAACT	TTAC			997
Db	898	GCCTGGAGTGT	TTCTAG	TCCC	ACTAG	TTGTT	GAACT	TTAC			938

RESULT 11									
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LOCUS	CS175725	560 bp	DNA	linear	PAT 12-OCT-2005				
DEFINITION	Sequence 3 from Patent WO2005090559.								
ACCESSION	CS175725								
VERSION	CS175725.1 GI:77627141								
KEYWORDS	.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;								

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1

ROHRSCHNEIDER, L.R.
Methods and compositions involving s-ship promoter regions
Patent: WO 2005090559-A 3 29-SEP-2005;
Fred Hutchinson Cancer Research Center (US)

FEATURES

Location/Qualifiers

source

1..560

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

ORIGIN

Query Match	51.8%;	Score 547.4;	DB 9;	Length 560;
Best Local Similarity	99.6%;			
Matches 559;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
Qy	456	CTCTGGGTTTCATCAAGAAACCCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT	515	
Db	1	CTCTGGGTTTCATCAAGAAACCCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT	60	
Qy	516	AATGTCAACCTCAAAACCCCTACCTGCATGTGCACACACACATACATCCACACACACACACA	575	
Db	61	AATGTCAACCTCAAAACCCCTACCTGCATGTGCACACACACATACATCCACACACACACA	120	
Qy	576	CAAATAAATAAATAA	635	
Db	121	CAAATAAATAAATAA	180	
Qy	636	AATATTTAGCTCTCCAGACCAAAATCTTGGTGAAACCCATGCATTTGTCATTTGTGTGTC	695	
Db	181	AATATTTAGCTCTCCAGACCAAAATCTTGGTGAAACCCATGCATTTGTCATTTGTGTGTC	240	

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Rohrschneider, L.R.
 TITLE Methods and compositions involving the s-ship promoter
 JOURNAL Patent: WO 2006102188-A 3 28-SEP-2006;
 Fred Hutchinson Cancer Research Center (US)

FEATURES
 source
 1..560
 /organism="Mus musculus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"

ORIGIN

Query Match	51.8%;	Score 547.4;	DB 9;	Length 560;
Best Local Similarity	99.6%;			
Matches 559;	Conservative	0;	Mismatches 1;	Indels 1; Gaps 1;

Qy	456	CTCTGGGTTTCATCAAGAAACCCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT	515
Db	1	CTCTGGGTTTCATCAAGAAACCCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT	60

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Db	241	CTACAAAACACTGAAGGTTAAGAAGCATGCTCCTTAGTAATTTATAGCAGTTTGCGTTTC	300
Qy	756	CAGATTGAAAAACAGATTCTATAGGCTACACAGTGCTAAATGGATTATGCTCAGATACAGA	815
Db	301	CAGATTGAAAAACAGATTCTATAGGCTACACAGTGCTAAATGGATTATGCTCAGATACAGA	360
Qy	816	TTGAAAAGGATACAGATTGAAAAGGGTCGGGGTCTGGGCCAGGATGACGGGCCAACTGAT	875
Db	361	TTGAAAAGGATACAGATTGAAAAGGGTCGGGGTCTGGGCCAGGATGACGGGCCAACT-AT	419
Qy	876	CTTTGCCGGGGCTTGTCCTTCAGGGAAGGTTACAGGATTCACCACTGGGGTGTGGCCTA	935
Db	420	CTTTGCCGGGGCTTGTCCTTCAGGGAAGGTTACAGGATTCACCACTGGGGTGTGGCCTA	479
Qy	936	TCTGCTGTTAGGACCTGAATTGCCCTGGAGTGTTTCTAGTTCCCAGTGTGTTGAACTTT	995
Db	480	TCTGCTGTTAGGACCTGAATTGCCCTGGAGTGTTTCTAGTTCCCAGTGTGTTGAACTTT	539
Qy	996	ACCTTGAAACCTCTGCTCCCAG	1016
Db	540	ACCTTGAAACCTCTGCTCCCAG	560

RESULT 13
AC102987

LOCUS AC102987 247782 bp DNA linear HTG 10-MAY-2003
DEFINITION Rattus norvegicus clone CH230-52N2, WORKING DRAFT SEQUENCE, 3

#####

unordered pieces.

AC102987

AC102987.5 GI:30521881

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 247782)

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

REFERENCE
AUTHORS
TITLE
JOURNAL

Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 247782)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On May 10, 2003 this sequence version replaced gi:23264611.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GHEE
Center clone name: CH230-52N2

----- Summary Statistics

Assembly program: Atlas 3.0;
Consensus quality: 237739 bases at least Q40
Consensus quality: 240323 bases at least Q30
Consensus quality: 242042 bases at least Q20

Estimated insert size: 247461; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 244348: contig of 244348 bp in length
* 244349 244448: gap of unknown length
* 244449 246420: contig of 1972 bp in length
* 246421 246520: gap of unknown length
* 246521 247782: contig of 1262 bp in length.

FEATURES

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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-52N2"

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clone_end:T7"

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ORIGIN

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Best Local Similarity	72.0%;								
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QY	1	CACTTCCAGCTTCCTTTATCA-TTTTAAAAAGAAATTTCCCTATGTGACTACTGTATTTAAA	59						
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QY	60	TCACCACACGGCCAATACTCCCCCCCCAACTCCTCCCAAATCCCCCTCTACCCCACTCAAAAT	119						
DB	146174	TCATTCCCCCTCCTGTACT-CCCTCCAACTCCTCCCCAAATCCCCCTCTACTCACTCAAAAT	146232						
QY	120	CTTATCTTGTATTCTTTATCATATTATACATATGTGTATATATGTGTGTGTATATAT	179						
DB	146233	TCGTGTGTATTATTATTATTGTTACATGTATGTACATATAAATATAT-----	146282						
QY	180	ATATACTATATACTGCTAATGAGTAACATTTAGTGTATTTCAT-TGTTGCATGTTTTC	238						
DB	146283	-----AAACGTAATCTGCCAATGAGTAACATTTAGTGTACTCATATGTTGCATGTTTAA	146337						
QY	239	AATGTGCTTTCAGGAGGCTGGGGGATGGCTCAGTGGGCAAAATTCAGCTGCACAAGC	298						
DB	146338	AATGTGCTTTCAGGAGGCTGGGGAGATGGCTCAGTGGGTAAGGTTCTTGTCTGCACAAAC	146397						

QY	299	CTAAGGACCAGGGTTCAGATCCCCA-----ATATAAAGGCTGGCTGGACATGGTGGCTT	352
Db	146398	CTAAGGACCAGGGTTCAGATCCCCCAATCAGCATAGAAAAGCTGGCTGGATGTGGTGGCTC	146457
QY	353	GCCTATGATACTAGCATGCTTGCTGGAAGCAAAGACAGGGAATCCCTGGAGACTTAGAAT	412
Db	146458	TCCTATGATACTAGCGTGTCTTTGGGAGCAAAGACGGGGAATCCCTAAAGACATGGAAT	146517
QY	413	CTCAGAAAGTGATCTGGGCTGGACAGACTAGCTGAACCTGGCCAGCTCTGGGTTTCATCAAGA	472
Db	146518	CTCTGAAGTGAGCT-GGCTGGACAGACTAGCTGAATCGACCAGCTCTGGGTTTCATCAAGA	146576
QY	473	AACCCCTACCTCCATAAACATAAAGTGTGATGGAGAAAAGGCACCTAATGTCAACCTCAAAAC	532
Db	146577	AACCCCTACCTCCATCA-----AGAGCGTGTATCACACCTAATGACAGCCTCAGGCC	146626
QY	533	CCTACCTGCATGTGCACACACATACATCCACACACACACACACACACACACACACAC	592
Db	146627	CCTACATGCATGTGCACACACATACATGCACACACACACAATAAGTTAATGAATAAAAT	146686
QY	593	ACACCACACACACACACACAAAAATAAAGTAAAT--AAATAAAATATTAGCTCTCC	650
Db	146687	ATTGGCTCTCCAGACCATAGTGAAACCTGGSCATTTGCATTTTTAGTGTGTGTGTGTGT	146746
QY	651	AGACCAAAATCTTGGTGAAACCCATGCATTTGCATTTGTGTGTGTCTACAAACACTGAAG	710
Db	146747	GtGT	146806
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Db	146807	TTTAAGAAAAATAGCTCCTAAGTAATTTTATAGTTGTTGTGTGTGTGTGTGTGTGTGTGT	146866

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Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 179418)

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G.,

Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
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 Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
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 Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
 Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
 Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
 Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE

Direct Submission

Unpublished

2 (bases 1 to 179418)

Worley,K.C.

Direct Submission

Submitted (07-MAR-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 179418)

Worley,K.C.

Direct Submission

Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Genome Center

COMMENT

```

Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXKG
Center clone name: CH230-195L1
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 139634 bases at least Q40
Consensus quality: 148988 bases at least Q30
Consensus quality: 156753 bases at least Q20
Estimated insert size: 145919; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*      1 1465: contig of 1465 bp in length
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*	14218	15454:	contig	of 1237	bp in length
*	15455	15554:	gap of	unknown	length
*	15555	17016:	contig	of 1462	bp in length
*	17017	17116:	gap of	unknown	length
*	17117	18499:	contig	of 1383	bp in length
*	18500	18599:	gap of	unknown	length
*	18600	19774:	contig	of 1175	bp in length
*	19775	19874:	gap of	unknown	length
*	19875	21219:	contig	of 1345	bp in length
*	21220	21319:	gap of	unknown	length
*	21320	22672:	contig	of 1353	bp in length
*	22673	22772:	gap of	unknown	length
*	22773	24752:	contig	of 1980	bp in length
*	24753	24852:	gap of	unknown	length
*	24853	26001:	contig	of 1149	bp in length
*	26002	26101:	gap of	unknown	length
*	26102	28650:	contig	of 2549	bp in length
*	28651	28750:	gap of	unknown	length
*	28751	30694:	contig	of 1944	bp in length
*	30695	30794:	gap of	unknown	length
+	30795	30894:	contig	of 1040	bp in length

*	30795	32634:	contig of 1840 bp in length
*	32635	32734:	gap of unknown length
*	32735	35068:	contig of 2334 bp in length
*	35069	35168:	gap of unknown length
*	35169	36796:	contig of 1628 bp in length
*	36797	36896:	gap of unknown length
*	36897	38190:	contig of 1294 bp in length
*	38191	38290:	gap of unknown length
*	38291	39461:	contig of 1171 bp in length
*	39462	39561:	gap of unknown length
*	39562	41210:	contig of 1649 bp in length
*	41211	41310:	gap of unknown length
*	41311	43224:	contig of 1914 bp in length
*	43225	43324:	gap of unknown length
*	43325	45608:	contig of 2284 bp in length
*	45609	45708:	gap of unknown length
*	45709	47065:	contig of 1357 bp in length
*	47066	47165:	gap of unknown length
*	47166	48454:	contig of 1289 bp in length
*	48455	48554:	gap of unknown length
*	48555	50246:	contig of 1692 bp in length
*	50247	50346:	gap of unknown length
*	50347	52037:	contig of 1691 bp in length
*	52038	52137:	gap of unknown length
*	52138	53888:	contig of 1751 bp in length
*	53889	53988:	gap of unknown length
*	53989	55344:	contig of 1356 bp in length
*	55345	55444:	gap of unknown length
*	55445	56683:	contig of 1239 bp in length
*	56684	56783:	gap of unknown length
*	56784	58824:	contig of 2041 bp in length
*	58825	58924:	gap of unknown length
*	58925	60588:	contig of 1664 bp in length
+	60589	60688:	contig of 1664 bp in length

*	60589	60688: gap of unknown length
*	60689	63023: contig of 2335 bp in length
*	63024	63123: gap of unknown length
*	63124	65633: contig of 2510 bp in length
*	65634	65733: gap of unknown length
*	65734	67706: contig of 1973 bp in length
*	67707	67806: gap of unknown length
*	67807	69538: contig of 1732 bp in length
*	69539	69638: gap of unknown length
*	69639	71035: contig of 1397 bp in length
*	71036	71135: gap of unknown length
*	71136	72415: contig of 1280 bp in length
*	72416	72515: gap of unknown length
*	72516	75179: contig of 2664 bp in length
*	75180	75279: gap of unknown length
*	75280	77087: contig of 1808 bp in length
*	77088	77187: gap of unknown length
*	77188	78940: contig of 1753 bp in length
*	78941	79040: gap of unknown length
*	79041	81122: contig of 2082 bp in length
*	81123	81222: gap of unknown length
*	81223	83707: contig of 2485 bp in length
*	83708	83807: gap of unknown length
*	83808	86713: contig of 2906 bp in length
*	86714	86813: gap of unknown length

Query Match		19.1%;	Score	201.2;	DB	4;	Length	179418;	
Best Local Similarity		81.0%;							
Matches	277;	Conservative	0;	Mismatches	48;	Indels	17;	Gaps	3;
Qy	230	CATGTTTTC	AATGTGCTT	CCAGGAGGCTGGGGG	GATGGCTCAGTGGG	CAAAATTC	TAGC	289	
Db	11317	CAATGTTTT	TCTGTGCTT	CCAGGAGGCTGGGG	GAGATGGCTCAGTGGG	TAAAGTTCT	TGC	11258	

QY	290	TGCACAAAGCCTAAAGGACCAGGGTTCAGATCCCCA-----ATATAAAGGCTGGCTGGACA	343
Db	11257	TGCACAAACCTAAGGACCAGGGTTCAGATCCCCCAATCAGCATAGAAAAGCTGGCTGGATG	11198
QY	344	TGGTGGCTTGCCCTATGATACTAGCATGCTTGCTGGAAGCAAAAGACAGGGAATCCCTGGAG	403
Db	11197	TGGTGGCTCTCCTATGATACTAGCGTGCTTGTGGGAGCAAAAGACGGGGAATCCCTAAAG	11138
QY	404	ACTTAGAATCTCAGAAAGTGATCTGGGCTGGACAGACTAGCTGAACTGGCCAGCTCTGGGT	463
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QY	464	TCATCAAGAAACCCCTACCTCCATAAACAATAAAAGTGTGATGGAGAAAGGCACCTAATGTCAA	523
Db	11078	TCATCAAGAAACCCCTACCTCCATCA-----AGAGCGTGATCACACCTAATGACAG	11029
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RESULT 15
 AC111472
 LOCUS AC111472 262016 bp DNA linear HTG 13-MAY-2003
 DEFINITION Rattus norvegicus clone CH230-82D4, WORKING DRAFT SEQUENCE.
 ACCESSION AC111472
 VERSION AC111472.5 GI:30579364
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Rodentia; Muridae; Murinae; Murinae; Murinae; Murinae

1 (bases 1 to 262016)

Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 262016)

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwaokenemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 262016)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 262016)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On May 13, 2003 this sequence version replaced gi:24942244.

the sequence in this submission is a combination of two bases

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GMJZ

Center clone name: CH230-82D4

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 245356 bases at least Q40

Consensus quality: 247686 bases at least Q30

Consensus quality: 249572 bases at least Q20

Estimated insert size: 257162; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

- * NOTE: Estimated insert size may differ from sequence length
- * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
- * NOTE: This sequence may represent more than one clone.
- * NOTE: This is a 'working draft' sequence. It currently
- * consists of 1 contigs. Gaps between the contigs
- + are represented as runs of Ns in the order of the clones

* are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 262016: contig of 262016 bp in length.

FEATURES

source

1. .262016
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-82D4"

misc_feature

1. .1000

/note="wgs_contig"

misc_feature

260556. .262016

/note="wgs_contig"

ORIGIN

Query Match	8.3%;	Score 87.8;	DB 4;	Length 262016;
Best Local Similarity	58.5%;			
Matches 210;	Conservative	0;	Mismatches 142;	Indels 7; Gaps 3;
Qy	235	TTTCAATGTGCTTTCCAGGAGGCTGGGGGGATGGCTCAGTGGGCAAAATTCTAGCTGCAC	294	
Db	4085	TCCTTTGGATCTCCACAGAGGGCTGGGTGATGGCATAATGGTAAAAAGCTCTCTATAT	4144	
Qy	295	AAGCCTAAGGACCAAGGTTTCAGATCCCCAATAATAAAGCTGGCTGGACATGGTGGCTTGC	354	
Db	4145	AAGCAGGAGGACCTGCGTTTGGATCCCCCAATGCACATGTAAAAGCCAAGTAGTGTCT	4204	
Qy	355	CTATGATACTAGCATGCTTGCTGGAAGCAAGACAGGGAATCCCTGGAGACTTAGAATCT	414	

Db	4205	GTAA-----TTGTAGCATTGAGGTCAAGGAAAGAGGTGGAGCAGGATGGGAGTGGGATCC	4259
Qy	415	CAGAAAGTGATCTGGGCTGGACAGACTAGCTGAACTGGCCAGCTCTGGGTTTCATCAAGAAA	474
Db	4260	CTAGGTCTTTGTAGGGATAGCTAGTCTA-TTGAATGGGGAGCTCTAGGTTTGATGAGAGA	4318
Qy	475	CCCTACCTCCATAAACATAAAAGTGTGATGGAGAAAGGCACCTAAATGTCAAACCTCAAAACCCC	534
Db	4319	CTCTGCTTCGAAAAAGTAAGAGAAATAATAGAGAAAGACACCAAAATATCGATCTCTTACTTC	4378
Qy	535	TACCTGCAATGTGCACACACATACATCCACACACACACACACACACACACACACA	593
Db	4379	CACATGTGCACGCGCACACACACACACACA-CACACACACACACACACACACACACA	4436

Search completed: June 16, 2010, 20:34:55
 Job time : 1427 secs